SEQUENCE LISTING

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atg	gat	att	ctt	tgt	gaa	gaa	aat	act	tct	ttg	agc	cca cor	Thr	Thr	Asn	40
Met	Asp	Ile	Leu		Glu	Glu	Asn	Thr	Ser 10	Leu	Ser	Ser	1111	15	ASII	
1				5					10					10		
tcc	cta	atg	caa	tta	aat	gat	gac	acc	agg	ctc	tac	agt	aat	gac	ttt	96
Ser	Leu	Met	Gln	Leu	Asn	Asp	Asp	Thr	Arg	Leu	Tyr	Ser	Asn	Asp	Phe	
			20					25					30			
aac	tcc	gga	gaa	gct	aac	act	tct	gat	gca	ttt	aac	tgg	aca	gtc	gac	144
Asn	Ser	Gly	Glu	Ala	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Trp	Thr	Val	Asp	
		35					40					45				
tct	gaa	aat	cga	acc	aac	ctt	tcc	tgt	gaa	ggg	tgc	ctc	tca	ccg	tcg	192
Ser	Glu	Asn	Arq	Thr	Asn	Leu	Ser	Cys	Glu	Gly	Cys	Leu	Ser	Pro	Ser	
	50		,			55					60					
.	a+ c	tcc	++=	c++	cat	ctic	cad	gaa	aaa	aac	tga	tct	gct	tta	ctg	24
cyc	T.eu	Ser	Leu	Leu	His	Leu	Gln	Glu	Lys	Asn	Trp	Ser	Āla	Leu	Leu	
65	neu	561			70				-	75					80	

Applicants: Hung-Teh Kao et al. Serial No: 09/929,313

Serial No: 09/929,313 Filed: August 14, 2001

Exhibit B

aca Thr	gcc Ala	gta Val	gtg Val	att Ile 85	att Ile	cta Leu	act Thr	att Ile	gct Ala 90	gga Gly	aac Asn	ata Ile	ctc Leu	gtc Val 95	atc Ile	288
atg Met	gca Ala	gtg Val	tcc Ser 100	cta Leu	gag Glu	aaa Lys	aag Lys	ctg Leu 105	cag Gln	aat Asn	gcc Ala	acc Thr	aac Asn 110	tat Tyr	ttc Phe	336
ctg Leu	atg Met	tca Ser 115	ctt Leu	gcc Ala	ata Ile	gct Ala	gat Asp 120	atg Met	ctg Leu	ctg Leu	ggt Gly	ttc Phe 125	ctt Leu	gtc Val	atg Met	384
ccc Pro	gtg Val 130	tcc Ser	atg Met	tta Leu	acc Thr	atc Ile 135	ctg Leu	tat Tyr	Gly	tac Tyr	cgg Arg 140	tgg Trp	cct Pro	ctg Leu	ccg Pro	432
agc Ser 145	aag Lys	ctt Leu	tgt Cys	gca Ala	gtc Val 150	tgg Trp	att	tac Tyr	ctg Leu	gac Asp 155	gtg Val	ctc	ttc Phe	tcc	acg Thr 160	480
gcc Ala	tcc Ser	atc Ile	atg Met	cac His 165	ctc Leu	tgc Cys	gcc Ala	atc Ile	tcg Ser 170	ctg Leu	gac Asp	cgc Arg	tac Tyr	gtc Val 175	gcc Ala	528
atc Ile	cag Gln	aat Asn	ccc Pro 180	atc Ile	cac	cac	agc Ser	cgc Arg 185	ttc Phe	aac Asn	tcc Ser	aga Arg	act Thr 190	aag Lys	gca Ala	576
ttt Phe	ctg Leu	aaa Lys 195	atc Ile	att Ile	gct Ala	gtt Val	tgg Trp 200	acc Thr	ata Ile	tca Ser	gta Val	ggt Gly 205	ata Ile	tcc Ser	atg Met	624
cca Pro	ata Ile 210	Pro	gtc Val	Phe	Gly	Leu	Gln	gac Asp	gat Asp	tcg Ser	aag Lys 220	Val	ttt Phe	aag I.ys	gag Glu	672
ggg Gly 225	Ser	tgc Cys	tta Leu	ctt Leu	gcc Ala 230	Asp	gat Asp	aac Asn	ttt Phe	gtc Val 235	Leu	atc Ile	ggc Gly	tct Ser	ttt Phe 240	720
gtg Val	tca Ser	ttt Phe	ttc Phe	att : Ile : 245	Pro	tta Leu	acc Thr	atc Ile	atg Met 250	Val	atc Ile	acc Thr	tac Tyr	ttt Phe 255	cta Leu	768
act Thr	ato	aag Lys	tca Ser 260	Leu	caç Glr	aaa Lys	gaa Glu	gct Ala 265	Thr	ttg Lev	ı tgt ı Cys	gta Val	agt Ser 270	Asp	ctt Leu	816

ggc	aca Thr	cgg Arg 275	gcc Ala	aaa Lys	tta Leu	gct Ala	tct Ser 280	ttc Phe	agc Ser	ttc Phe	ctc Leu	cct Pro 285	cag Gln	agt Ser	tct Ser	864
			gaa Glu													912
tcc Ser 305	tac Tyr	aca Thr	ggc	agg Arg	agg Arg 310	act Thr	atg Met	cag Gln	tcc Ser	atc Ile 315	agc Ser	aat Asn	gag Glu	caa Gln	aag Lys 320	960
gca Ala	tgc Cys	aag Lys	gtg Val	ctg Leu 325	ggc Gly	atc Ile	gtc Val	ttc Phe	ttc Phe 330	ctg Leu	ttt Phe	gtg Val	gtg Val	atg Met 335	tgg Trp	1008
			ttc Phe 340													1056
			gat Asp													1104
			tct Ser													1152
aag Lys 385	acc Thr	tat Tyr	agg Arg	tca Ser	gcc Ala 390	ttt Phe	tca Ser	cgg Arg	tat Tyr	att Ile 395	cag Gln	tgt Cys	cag Gln	tac Tyr	aag Lys 400	1200
			aaa Lys					Ile		Val						1248
ttg Leu	gcc Ala	tac Tyr	aag Lys 420	tct Ser	agc Ser	caa Gln	ctt Leu	caa Gln 425	atg Met	gga Gly	caa Gln	aaa Lys	aag Lys 430	aat Asn	tca Ser	1296
aag Lys	caa Gln	gat Asp 435	gcc Ala	aag Lys	aca Thr	aca Thr	gat Asp 440	aat Asn	gac Asp	tgc Cys	tca Ser	atg Met 445	gtt Val	gct Ala	cta Leu	1344
gga Gly	aag Lys 450	Gln	cat His	tct Ser	gaa Glu	gag Glu 455	gct Ala	tct Ser	aaa Lys	gac Asp	aat Asn 460	Ser	gac Asp	gga Gly	gtg Val	1392
							3									

aat gaa aag gtg agc tgt gtg tga tag gct agt tgc cgt ggc aac tgt Ala Ser Cys Arg Gly Asn Cys Asn Glu Lys Val Ser Cys Val 475 470 465 ggaaggcaca ctgagcaagt tttcacctat ctggtttttt ttg <210> 2 <211> 471 <212> PRT <213> Homo sapiens <400> 2 Met Asp Ile Leu Cys Glu Glu Asn Thr Ser Leu Ser Ser Thr Thr Asn 10 Ser Leu Met Gln Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn Asp Phe 25 20 Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val Asp 40 45 35 Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser 55 Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu 70 Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile 90 85 Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe 105 100 Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met 125 120 Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro 135 Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr 150 155 Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala 170 165 Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala 190 185 .180 Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met 205 195 Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu 220 215 Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe 235 230 Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu 245 250 Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu 265 Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser

285 280 275 Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly 300 295 Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys 315 310 Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp 330 325 Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser 345 340 Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile 360 355 Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn 380 375 Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys 395 390 Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala 405 410 Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser 425 430 420 Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu 440 435 Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val 460 455 Asn Glu Lys Val Ser Cys Val 470 465

<210> 3 <211> 7 <212> PRT <213> Homo sapiens <400> 3 Ala Ser Cys Arg Gly Asn Cys

<210> 4 <211> 471 <212> PRT <213> Rattus norvegicus

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1 5 10 15

Ser Leu Met Asp Leu Gly Asp Gly Pro Ala Leu Val His Asn Asp Phe

25

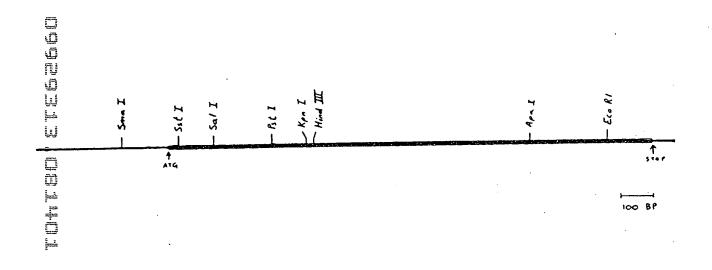
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Asn Ser Arg Asp Ala Asn Thr Ser Glu Ala Ser Asn Trp Thr Ile Asp 35 40 45

- Ala Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Tyr Leu Pro Pro Thr 50 55 60
- Cys Leu Ser Ile Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu 65 70 75 80
- Thr Thr Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile 85 90 95
- Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe 100 105 110
- Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met 115 120 125
- Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro 130 135 140
- Ser Lys Leu Cys Ala Ile Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr 145 150 155 160
- Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala 165 170 175
- Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala 180 185 190
- Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met 195 200 205
- Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu 210 215 220
- Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe 225 230 235 240
- Val Ala Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu 245 250 255
- Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu 260 265 270
- Ser Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser

275 280

Leu	Ser 290	Ser	Glu	Lys	Leu	Phe 295	Gln	Arg	Ser	Ile	His 300	Arg	Glu	Pro	Gly
Ser 305	Tyr	Ala	Gly	Arg	Arg 310	Thr	Met	Gln	Ser	Ile 315	Ser	Asn	Glu	Gln	Lys 320
Ala	Cys	Lys	Val	Leu 325	Gly	Ile	Val	Phe	Phe 330	Leu	Phe	Val	Val	Met 335	Trp
Cys	Pro	Phe	Phe 340	Ile	Thr	Asn	Ile	Met 345	Ala	Val	Ile	Cys	Lys 350	Glu	Ser
Cys	Asn	Glu 355	Asn	Val	Ile	Gly	Ala 360	Leu	Leu	Asn	Val	Phe 365	Val	Trp	Ile
Gly	Tyr 370	Leu	Ser	Ser	Ala	Val 375	Asn	Pro	Leu	Val	Tyr 380	Thr	Leu	Phe	Asn
Lys 385	Thr	Tyr	Arg	Ser	Ala 390	Phe	Ser	Arg	Tyr	Ile 395	Gln	Cys	Gln	Tyr	Lys 400
Glu	Asn	Arg	Lys	Pro 405	Leu	Gln	Leu	Ile	Leu 410	Val	Asn	Thr		Pro 415	Ala
Leu	Ala	Tyr	Lys 420	Ser	Ser	Gln	Leu	Gln 425	Val	Gly	Gln	Lys	Lys 430	Asn	Ser
Gln	Glu	Asp 435	Ala	Glu	Gln	Thr	Val 440	Asp	Asp	Cys	Ser	Met 445	Val	Thr	Leu
Gly	Lys 450	Gln	Gln	Ser	Glu	Glu 455	Asn	Cys	Thr	Asp	Asn 460		Glu	Thr	Val
Asn 465	Glu	Lys	Val	Ser	Cys 470	Val									



2/10 FIGURE 2

Met Asp Ile Leu Cys Glu Glu Asn Thr <u>ATGGATATTCTTGTGAAGAAAAT</u>ACTTCT 10 20 30 Leu Ser Thr Thr Asn Ser Leu Met Gln Ser TET G A G C T C A A C T A C G A A C T C C C T A A T G C A A 40 50 60 Ū Ш Asn Asp Asp Thr Arg Leu Tyr Ser T T A A A T G A T G A C A C C A G G C T C T A C A G T A A T 70 90 80 Ō **j** Phe Asn Ser Gly Glu Ala Asn Thr GA CTTTAACTCCGGAGAAGCTAACACTTCT 100 110 120 Ala Phe Asn Trp Thr Val Asp Ser Glu GATGCATTTAACTGGACAGTCGACTCAAA 130 140 150 Leu Ser Cys Glu Gly Cys Asn Arq Thr Asn

A A T C G A A C C A A C C T T T C C T G T G A A G G G T G C

170

160

3/10 FIGURE 2, CON'D

Leu Ser Pro Ser Cys Leu Ser Leu Leu His CTCTCACCGTCGTGTCTCTCTTACTTCAT
190 200 210

Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu CTCCAGGAAAAAACTGGTCTGCTTTACTG
220 230 240

Thr Ala Val Val Ile Ile Leu Thr Ile Ala

ACAGCCGTAGTGATTATTCTAACTATTGCT

250 260 270

Gly Asn Ile Leu Val Ile Met Ala Val Ser GGAAACATACTCGTCATCATGGCAGTGTCC 280 290 300

Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn CTAGAGAAAAAGCTGCAGAATGCCACCAAC
310 320 330

Tyr Phe Leu Met Ser Leu Ala Ile Ala Asp
TATTTCCTGATGTCACTTGCCATAGCTGAT
340 350 360

Met Leu Leu Gly Phe Leu Val Met Pro Val ATGCTGCTGGGTTTCCTTGTCATGCCCGTG 370 380 390

Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg
T C C A T G T T A A C C A T C C T G T A T G G G T A C C G G
400 410 420

Trp Pro Leu Pro Ser Lys Leu Cys Ala Val TGGCCTCTGCCGAGCAAGCTTTGTGCAGTC 430 440 450

Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr
TGGATTTACCTGGACGTGCTCTTCTCACG
460 470 480

Ala Ser Ile Met His Leu Cys Ala Ile Ser GCCTCCATCATGCACCTCTGCGCCATCTCG 490 500 510

Teu Asp Arg Tyr Val Ala Ile Gln Asn Pro
TGGACCGCTACGTCGCCATCCAGAATCCC

520
540

Ш

Tile His His Ser Arg Phe Asn Ser Arg Thr
ATCCACCACAGCCGCTTCAACTCCAGAACT

550
570

Lys Ala Phe Leu Lys Ile Ile Ala Val Trp
AAGGCATTTCTGAAAATCATTGCTGTTTGG
580 590 600

Thr Ile Ser Val Gly Ile Ser Met Pro Ile
ACCATATCAGTAGGTATATCCATGCCAATA
610 620 630

Pro Val Phe Gly Leu Gln Asp Asp Ser Lys
CCAGTCTTTGGGCTACAGGACGATTCGAAG
640 650 660

Val Phe Lys Glu Gly Ser Cys Leu Leu Ala GTCTTTAAGGAGGGGAGTTGCTTACTTGCC 670 680 690

Asp Asp Asn Phe Val Leu Ile Gly Ser Phe GATGATAACTTTGTCCTGATCGGCTCTTTT
700 710 720

ValSerPhePheIleProLeuThrIleMetGTGTCATTTCATTCCTTTAACCATG730740750

Tal Ile Thr Tyr Phe Leu Thr Ile Lys Ser TGATCACCTACTTTCTAACTATCAAGTCA
760 770 780

Leu Gln Lys Glu Ala Thr Leu Cys Val Ser CTCCAGAAAGAAGCTACTTTGTGTGTAAGT
790 800 810

ũ

Asp Leu Gly Thr Arg Ala Lys Leu Ala Ser

ATCTTGGCACACGGGCCAAATTAGCTTCT

820
830
840

Phe Ser Phe Leu Pro Gln Ser Ser Leu Ser
TTCAGCTTCCTCCTCAGAGTTCTTTGTCT
850 860 870

Ser Glu Lys Leu Phe Gln Arg Ser Ile His T C A G A A A G C T C T T C C A G C G T C G A T C C A T 880 890 900

Arg Glu Pro Gly Ser Tyr Thr Gly Arg Arg
A G G G A G C A G G G T C C T A C A C A G G C A G G A G G
910 920 930

Thr Met Gln Ser Ile Ser Asn Glu Gln Lys

A C T A T G C A G T C C A T C A G C A A T G A G C A A A A G

940 950 960

Ala Cys Lys Val Leu Gly Ile Val Phe Phe
-G-C-A-T-G-C-A-A-G-G-T-G-G-G-C-A-T-C-G-T-C-T-T-C
970 980 990

Leu Phe Val Val Met Trp Cys Pro Phe Phe Cr G T T T G T G G T G G T G G C C C T T T C

Ile Thr Asn Ile Met Ala Val Ile Cys Lys

ATCACAAACATCATGGCCGTCATCTGCAAA

1030 1040 1050

Glu Ser Cys Asn Glu Asp Val Ile Gly Ala
G A G T C C T G C A A T G A G G A T G T C A T T G G G G C C

1060 1070 1080

Leu Leu Asn Val Phe Val Trp Ile Gly Tyr
CTGCTCAATGTGTTTTGGATCGGTTAT
1090 1100 1110

Leu Ser Ser Ala Val Asn Pro Leu Val Tyr
C T C T C T C A G C A G T C A A C C C A C T A G T C T A C
1120 1130 1140

Thr Leu Phe Asn Lys Thr Tyr Arg Ser Ala
A C A C T G T T C A A C A A G A C C T A T A G G T C A G C C

1150 1160 1170

Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys
T T T T C A C G G T A T A T T C A G T G T C A G T A C A A G
1180 1190 1200

Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu

GAAAACAAAACCATTGCAGTTAATTTA

1210 1220 1230

Tal Asn Thr Ile Pro Ala Leu Ala Tyr Lys TGAACACAATACCGGCTTTGGCCTACAAG

1240 1250 1260

Ser Ser Gln Leu Gln Met Gly Gln Lys Lys The CTAGCCAACTTCAAATGGGACAAAAAAG
1270 1280 1290

Asn Ser Lys Gln Asp Ala Lys Thr Thr Asp
ATTCAAAGCAAGATGCCAAGACAACAGAT

1300 1310 1320

Õ

Asn Asp Cys Ser Met Val Ala Leu Gly Lys
A A T G A C T G C T C A A T G G T T G C T C T A G G A A A G

1330 1340 1350

Gln His Ser Glu Glu Ala Ser Lys Asp Asn C A G C A T T C T G A A G A G G C T T C T A A A G A C A A T 1360 1370 1380

Ser Asp Gly Val Asn Glu Lys Val Ser Cys AGCGACGGAGTGAATGAAAGGTGAGCTGT 1390 1400 1410

Val *** *** Ala Ser Cys Arg Gly Asn Cys G T G T G A T A G G C T A G T T G C C G T G G C A A C T G T 1420 1430 1440

G G A A G G C A C A C T G A G C A A G T T T T C A C C T A T

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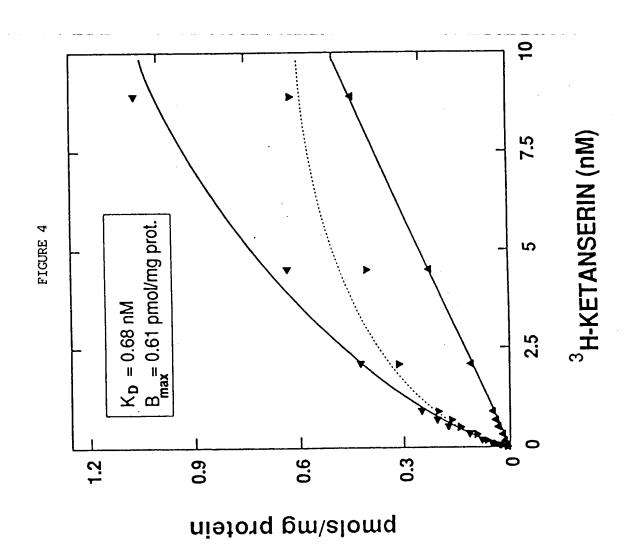
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1480

1480

9/10

TCHTEO CTCCCC



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